

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Ken-ichi Nakayama et al. Art Unit : Unknown
Serial No. : 10/089,014 Examiner : Unknown
Filed : March 25, 2002
Title : GDP-4-KETO-6-DEOXY-D-MANNOSE-3, 5-EPIMERASE-4-REDUCTASE
 GENE DERIVED FROM ARABIDOPSIS THALIANA

BOX PCT


Commissioner for Patents
Washington, DC 20231

VERIFIED STATEMENT UNDER 37 CFR §1.821(f)

I, Katica Magovcevic, declare that I personally prepared the paper and the computer-readable copy of the Sequence Listing filed herewith for the above-identified application and that the content of both is the same.

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of The United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: 7/8/02


Katica Magovcevic

Fish & Richardson P.C.
225 Franklin Street
Boston, Massachusetts 02110-2804
(617) 542-5070 telephone
(617) 542-8906 facsimile

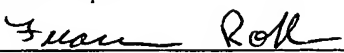
20463225.doc

CERTIFICATE OF MAILING BY EXPRESS MAIL

Express Mail Label No. EF3538167570J

I hereby certify under 37 CFR §1.10 that this correspondence is being deposited with the United States Postal Service as Express Mail Post Office to Addressee with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, Washington, D.C. 20231.

July 25 - 2002
Date of Deposit


Signature

Francisco Robles
Typed or Printed Name of Person Signing Certificate

SEQUENCE LISTING

<110> Nakayama, Ken-ichi
Jigami, Yoshifumi

<120> GDP-4-KETO-6-DEOXY-D-MANNOSE-3,
5-EPIMERASE-4-REDUCTASE GENE DERIVED FROM ARABIDOPSIS
THALIANA

<130> 11283-019US1

<140> US 10/089,014

<141> 2002-03-05

<150> PCT/JP00/02049

<151> 2000-03-30

<150> JP 329045/1999

<151> 1999-11-19

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 312

<212> PRT

<213> Arabidopsis thaliana

<400> 1

Met	Ser	Asp	Lys	Ser	Ala	Lys	Ile	Phe	Val	Ala	Gly	His	Arg	Gly	Leu
1				5					10					15	
Val	Gly	Ser	Ala	Ile	Val	Arg	Lys	Leu	Gln	Glu	Gln	Gly	Phe	Thr	Asn
			20					25					30		
Leu	Val	Leu	Lys	Thr	His	Ala	Glu	Leu	Asp	Leu	Thr	Arg	Gln	Ala	Asp
		35					40					45			
Val	Glu	Ser	Phe	Phe	Ser	Gln	Glu	Lys	Pro	Val	Tyr	Val	Ile	Leu	Ala
	50					55					60				
Ala	Ala	Lys	Val	Gly	Gly	Ile	His	Ala	Asn	Asn	Thr	Tyr	Pro	Ala	Asp
65					70					75					80
Phe	Ile	Gly	Val	Asn	Leu	Gln	Ile	Gln	Thr	Asn	Val	Ile	His	Ser	Ala
				85					90					95	
Tyr	Glu	His	Gly	Val	Lys	Lys	Leu	Leu	Phe	Leu	Gly	Ser	Ser	Cys	Ile
			100					105					110		
Tyr	Pro	Lys	Phe	Ala	Pro	Gln	Pro	Ile	Pro	Glu	Ser	Ala	Leu	Leu	Thr
		115					120					125			
Ala	Ser	Leu	Glu	Pro	Thr	Asn	Glu	Trp	Tyr	Ala	Ile	Ala	Lys	Ile	Ala
		130				135					140				
Gly	Ile	Lys	Thr	Cys	Gln	Ala	Tyr	Arg	Ile	Gln	His	Gly	Trp	Asp	Ala
145					150					155					160
Ile	Ser	Gly	Met	Pro	Thr	Asn	Leu	Tyr	Gly	Pro	Asn	Asp	Asn	Phe	His
			165						170					175	
Pro	Glu	Asn	Ser	His	Val	Leu	Pro	Ala	Leu	Met	Arg	Arg	Phe	His	Glu
			180					185					190		
Ala	Lys	Val	Asn	Gly	Ala	Glu	Glu	Val	Val	Val	Trp	Gly	Thr	Gly	Ser
			195				200						205		

Pro Leu Arg Glu Phe Leu His Val Asp Asp Leu Ala Asp Ala Cys Val
 210 215 220
 Phe Leu Leu Asp Arg Tyr Ser Gly Leu Glu His Val Asn Ile Gly Ser
 225 230 235 240
 Gly Gln Glu Val Thr Ile Arg Glu Leu Ala Glu Leu Val Lys Glu Val
 245 250 255
 Val Gly Phe Glu Gly Lys Leu Gly Trp Asp Cys Thr Lys Pro Asp Gly
 260 265 270
 Thr Pro Arg Lys Leu Met Asp Ser Lys Leu Ala Ser Leu Gly Trp
 275 280 285
 Thr Pro Lys Val Ser Leu Arg Asp Gly Leu Ser Gln Thr Tyr Asp Trp
 290 295 300
 Tyr Leu Lys Asn Val Cys Asn Arg
 305 310

<210> 2

<211> 936

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)...(936)

<400> 2

atg tct gac aaa tct gcc aaa atc ttc gtc gcg ggt cat cgt ggt ttg 48
 Met Ser Asp Lys Ser Ala Lys Ile Phe Val Ala Gly His Arg Gly Leu
 1 5 10 15

gtt gga tct gcc att gtc cgc aag ctt cag gaa caa ggt ttc acc aat 96
 Val Gly Ser Ala Ile Val Arg Lys Leu Gln Glu Gln Gly Phe Thr Asn
 20 25 30

ctc gtt ctt aaa aca cac gcc gag ctt gat ctc act cgt caa gcc gat 144
 Leu Val Leu Lys Thr His Ala Glu Leu Asp Leu Thr Arg Gln Ala Asp
 35 40 45

gtt gaa tcc ttc ttt tct caa gag aag cca gtt tat gta atc cta gca 192
 Val Glu Ser Phe Phe Ser Gln Glu Lys Pro Val Tyr Val Ile Leu Ala
 50 55 60

gca gct aaa gtt ggt ggt att cac gct aac aac acc tat cct gct gat 240
 Ala Ala Lys Val Gly Gly Ile His Ala Asn Asn Thr Tyr Pro Ala Asp
 65 70 75 80

ttc att ggt gtc aat ctc cag att cag acc aat gtg atc cac tct gca 288
 Phe Ile Gly Val Asn Leu Gln Ile Gln Thr Asn Val Ile His Ser Ala
 85 90 95

tat gag cac ggt gtg aag aag ctt ctc ttc ctt gga tca tcc tgc att 336
 Tyr Glu His Gly Val Lys Lys Leu Leu Phe Leu Gly Ser Ser Cys Ile
 100 105 110

tac cct aaa ttt gct cct cag cca att cct gag tct gct ttg tta aca 384
 Tyr Pro Lys Phe Ala Pro Gln Pro Ile Pro Glu Ser Ala Leu Leu Thr
 115 120 125

gca tcg ctt gaa cca act aat gag tgg tat gct att gct aag atc gct Ala Ser Leu Glu Pro Thr Asn Glu Trp Tyr Ala Ile Ala Lys Ile Ala 130 135 140	432
ggg att aag act tgt cag gct tat agg att cag cac gga tgg gat gca Gly Ile Lys Thr Cys Gln Ala Tyr Arg Ile Gln His Gly Trp Asp Ala 145 150 155 160	480
atc tct ggc atg cct act aat ctc tat ggt cct aat gac aat ttc cac Ile Ser Gly Met Pro Thr Asn Leu Tyr Gly Pro Asn Asp Asn Phe His 165 170 175	528
ccg gag aat tct cat gtg ctt cct gct ctt atg agg agg ttc cac gag Pro Glu Asn Ser His Val Leu Pro Ala Leu Met Arg Arg Phe His Glu 180 185 190	576
gcg aaa gtg aat gga gcg gag gaa gtt gtg gtg tgg ggt aca ggt agt Ala Lys Val Asn Gly Ala Glu Glu Val Val Val Trp Gly Thr Gly Ser 195 200 205	624
ccg ttg agg gag ttc ttg cat gtt gat gat ttg gct gat gct tgt gtt Pro Leu Arg Glu Phe Leu His Val Asp Asp Leu Ala Asp Ala Cys Val 210 215 220	672
ttc ttg ctg gat cga tac agc ggg ttg gag cat gtt aac att gga agt Phe Leu Leu Asp Arg Tyr Ser Gly Leu Glu His Val Asn Ile Gly Ser 225 230 235 240	720
ggt caa gaa gtg act att aga gag ttg gct gag ttg gtg aaa gag gtt Gly Gln Glu Val Thr Ile Arg Glu Leu Ala Glu Leu Val Lys Glu Val 245 250 255	768
ggt ggt ttt gaa ggg aag ctt gga tgg gat tgc act aag cca gat ggc Val Gly Phe Glu Gly Lys Leu Gly Trp Asp Cys Thr Lys Pro Asp Gly 260 265 270	816
aca ccg agg aaa ctt atg gac agc tca aag ctc gcg tct ttg ggt tgg Thr Pro Arg Lys Leu Met Asp Ser Ser Lys Leu Ala Ser Leu Gly Trp 275 280 285	864
aca cct aag gtt tct ctt aga gat ggt ctg agc caa act tat gat tgg Thr Pro Lys Val Ser Leu Arg Asp Gly Leu Ser Gln Thr Tyr Asp Trp 290 295 300	912
tat ttg aag aat gtt tgc aac cga Tyr Leu Lys Asn Val Cys Asn Arg 305 310	936

<210> 3

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 3

attggtacca tgtctgacaa atctgccaaa atcttcgtc 39

<210> 4

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 4

ttagtcgacg atatctcggg tgcaaacatt cttcaaatac caatcataag 50

<210> 5

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 5

gtcgaattca tggcgtcaga gaacaac 27

<210> 6

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 6

gaactcgaga gggtgctgct tagcatc 27